

AMENDMENTS TO THE SPECIFICATION

The following paragraphs [00207], [00369], and [00421] will replace all prior versions of paragraphs [00207], [00369], and [00421] in this application:

[00207] In general, techniques for identifying aptamers involve incubating a preselected non-nucleic acid target molecule with mixtures (2 to 50 members), pools (50 to 5,000 members) or libraries (50 or more members) of different nucleic acids that are potential aptamers under conditions that allow complexes of target molecules and aptamers to form. By “different nucleic acids” it is meant that the nucleotide sequence of each potential aptamer may be different from that of any other member, that is, the sequences of the potential aptamers are random with respect to each other. Randomness can be introduced in a variety of manners such as, *e.g.*, mutagenesis, which can be carried out *in vivo* by exposing cells harboring a nucleic acid with mutagenic agents, *in vitro* by chemical treatment of a nucleic acid, or *in vitro* by biochemical replication (*e.g.*, PCR) that is deliberately allowed to proceed under conditions that reduce fidelity of replication process; randomized chemical synthesis, *i.e.*, by synthesizing a plurality of nucleic acids having a preselected sequence that, with regards to at least one position in the sequence, is random. By “random at a position in a preselected sequence” it is meant that a position in a sequence that is normally synthesized as, *e.g.*, as close to 100% A as possible (*e.g.*, 5'-C-T-T-A-G-T-3') (SEQ ID NO:1), is allowed to be randomly synthesized at that position (C-T-T-N-G-T, wherein N indicates a randomized position) (SEQ ID NO:2). At a randomized position, for example, the synthesizing reaction contains 25% each of A,T,C and G; or x % A, w % T, y % C and z % G, wherein x+w+y+z=100. The randomization at the position may be complete (*i.e.*, x=y=w=z=25%) or stochastic (*i.e.*, at least one of x, w, y and z is not 25%).

[00369] Nuclear factor kappa B (NF-κB) is a dimeric protein complex occurring in many tissue cells and in particular in blood cells. NF-κB takes on a particular role in the control of the expression of genes which have an NF-κB binding sequence (5'-GGG^uNNP^yP^yCC-3') (SEQ ID NO: 3) in their promoter sequence. To this extent, NF-κB is a transcription factor. The physiological activity of NF-κB in the control of gene expression, however, is subject to a regulation principle, in which NF-κB is released from a complex with proteins of the I_κB class in order to be translocated as a transcription factor to the cell nucleus resulting in gene activation. The regulation principle for the release of active NF-κB from a complex with the protein I_κB is still not known in detail.

[00421] The NF-κB decoy that can be used in the present invention may be any compound that specifically antagonizes the NF-κB binding site of the chromosomes and includes but is not limited to nucleic acids and their analogs. As preferred examples of the NF-κB decoy, the present invention may utilize NF-κB decoy comprising one or more copies of oligonucleotides CCTTGAAGGGATTCCCTCC (SEQ ID NO: 4) and GGAACCTTCCCTAAAGGGAGG (SEQ ID NO: 5), preferably, the NF-κB decoy are described as oligonucleotides containing the nucleotide sequence of GGGATTCCCC (SEQ ID NO: 6). Preferably, the NF-κB decoy oligonucleotide is a double-stranded 22 bp oligonucleotide (5'-AGTTGAGGGACTTCCCAGGC-3') (SEQ ID NO: 7) (Promega).